- 1 -

SEQUENCE LISTING

```
        <110>  AstraZeneca AB

  5     <120>  Molecules

        <130>  CCH/100852

        <150>  GB 0306185
 10     <151>  2003-03-19

        <160>  1

        <170>  PatentIn version 3.2
 15
        <210>  1
        <211>  2986
        <212>  DNA
        <213>  Homo sapiens
 20
        <400>  1
        ctgaaaacag aagatagaga ggagtctcgg agctcgccat ctccagcgat ctctacattg      60
        ggaaaaaaca tggagtcagc tccggcagcc cccgaccccg ccgccagcga gccaggcagc     120
        agcggcgcgg acgcggccgc cggctccagg gagaccccgc tgaaccagga atccgcccgc     180
 25     aagagcgagc cgcctgcccc ggtgcgcaga cagagctatt ccagcaccag cagagatgat     240
        gactttttc atgaactccc agaaactttt ccttctgatc cacctgagcc tctgccacat     300
        ttccttattg agcctgaaga agcttatatt gtgaagaata agcctgtgaa cctgtactgt     360
        aaagcaagcc ctgccaccca gatctatttc aagtgtaata gtgaatgggt tcatcagaag     420
        gaccacatag tagatgaaag agtagatgaa acttccggtc tcattgtccg ggaagtgagc     480
 30     attgagattt cgcgcagca agtggaagaa ctctttggac ctgaagatta ctggtgccag     540
        tgtgtggcct ggagctccgc gggtaccaca aagagccgga aggcgtatgt gcgcattgca     600
        tatctacgga agacatttga gcaggaaccc ctaggaaagg aagtgtcttt ggaacaggaa     660
        gtcttactcc agtgtcgacc acctgaaggg atcccagtgg ctgaggtgga atggttgaaa     720
        aatgaagaca taattgatcc cgttgaagat cggaattttt atattactat tgatcacaac     780
 35     ctcatcataa agcaggcccg actctctgat actgcaaatt acacctgtgt tgccaaaaac     840
        attgttgcca agaggaaaag tacaactgcc actgtcatag tctatgtcaa cggtggctgg     900
        tccacctgga cggagtggtc tgtgtgtaac agccgctgtg acgagggta tcagaaacgt     960
        acaaggactt gtaccaaccc ggcaccactc aatgggggtg ccttctgtga agggcagagt    1020
        gtgcagaaaa tagcctgtac tacgttatgc ccagtggatg gcaggtggc gccatggagc    1080
 40     aagtggtcta cttgtggaac tgagtgcacc cactggcgca ggaggggagtg cacggcgcca    1140
        gcccccaaga atggaggcaga ggactgcgac ggcctcgtct tgcaatccaa gaactgcact    1200
        gatgggctt gcatgcagag tttcattta tcccattca ctgaacagag aacccagaat    1260
        gaatatggat ttctttcgc tcctgattca gatgatgttg ctctctatgt tgggattgtg    1320
        atagcagtga tcgtttgcct ggcgatctct gtagttgtgg ccttgtttgt gtatcggaag    1380
 45     aatcatcgtg actttgagtc agatattatt gactcttcgg cactcaatgg gggctttcag    1440
        cctgtgaaca tcaaggcagc aagacaagat ctgctggctg taccccaga cctcacgtca    1500
        gctgcagcca tgtacagagg acctgtctat gccctgcatg acgtctcaga caaaatccca    1560
        atgaccaact ctccaattct ggatccactg cccaacctga aaatcaaagt gtacaacacc    1620
        tcaggtgctg tcacccccca agatgacctc tctgagttta cgtccaagct gtccctcag    1680
 50     atgacccagt cgttgttgga gaatgaagcc ctcagcctga gaaccagag tctagcaagg    1740
        cagactgatc catcctgtac cgcatttggc agcttcaact cactgggagg tcaccttatt    1800
        gttcccaatt caggagtcag cttgctgatt cccgctgggg ccattcccca aggggagagtc    1860
        tacgaaatgt atgtgacctgt acacaggaaa gaaactatga ggccacccat ggatgactct    1920
        cagacacttt tgacccctgt ggtgagctgt gggcccccag gagctctgct caccgcgcccc    1980
 55     gtcgtcctca ctatgcatca ctgcgcagac cccaataccg aggactggaa aatactgctc    2040
        aagaaccagg cagcacaggg acagtgggag gatgtggtgg tggtcgggga ggaaaacttc    2100
        accacccct gctacattca gctggatgca gaggcctgcc acatcctcac agagaacctc    2160
        agcacctacg ccctggtagg acattccacc accaaagcgg ctgcaaagcg cctcaagctg    2220
        gccatctttg ggcccctgtg ctgctcctcg ctggagtaca gcatccgagt ctactgtctg    2280
 60     gatgacaccc aggatgccct gaaggaaatt ttacatcttg agagacagac gggaggacag    2340
        ctcctagaag aacctaaggc tcttcatttt aaaggcagca cccacaacct gcgcctgtca    2400
        attcacgata tcgcccattc cctctggaag agcaaattgc tggctaaata tcaggaaatt    2460
        ccattttacc atgtttggag tggatctcaa agaaacctgc actgcacctt cactctggaa    2520
        agatttagcc tgaacacagt ggagctggtt tgcaaactct gtgtgcggca ggtggaagga    2580
 65     gaagggcaga tcttccagct caactgcacc gtgtcagagg aacctactgg catcgatttg    2640
        ccgctgctgg atcctgcgaa caccatcacc acggtcacgg ggcccagtgc tttcagcatc    2700
        cctctcccta tccggcagaa gctctgtagc agcctggatg ccccccagac gagaggccat    2760
        gactggagga tgctggccca taagctgaac ctggacaggt acttgaatta ctttgccacc    2820
```

```
aaatccagcc caactggcgt aatcctggat ctttgggaag cacagaactt cccagatgga    2880
aacctgagca tgctggcagc tgtcttggaa gaaatgggaa gacatgaaac ggtggtgtcc    2940
ttagcagcag aagggcagta ttaaccacca tgctggaagg ggaaat                   2986
```

5

<210> 2
<211> 964
<212> PRT
<213> Homo sapiens

10

<400> 2

Met Glu Ser Ala Pro Ala Ala Pro Asp Pro Ala Ala Ser Glu Pro Gly
 1   5   10   15

Ser Ser Gly Ala Asp Ala Ala Ala Gly Ser Arg Glu Thr Pro Leu Asn
            20   25   30

Gln Glu Ser Ala Arg Lys Ser Glu Pro Pro Ala Pro Val Arg Arg Gln
            35   40   45

Ser Tyr Ser Ser Thr Ser Arg Asp Asp Asp Phe Phe His Glu Leu Pro
        50   55   60

Glu Thr Phe Pro Ser Asp Pro Pro Glu Pro Leu Pro His Phe Leu Ile
 65   70   75   80

Glu Pro Glu Glu Ala Tyr Ile Val Lys Asn Lys Pro Val Asn Leu Tyr
                85   90   95

Cys Lys Ala Ser Pro Ala Thr Gln Ile Tyr Phe Lys Cys Asn Ser Glu
            100   105   110

Trp Val His Gln Lys Asp His Ile Val Asp Glu Arg Val Asp Glu Thr
        115   120   125

Ser Gly Leu Ile Val Arg Glu Val Ser Ile Glu Ile Ser Arg Gln Gln
    130   135   140

Val Glu Glu Leu Phe Gly Pro Glu Asp Tyr Trp Cys Gln Cys Val Ala
145   150   155   160

Trp Ser Ser Ala Gly Thr Thr Lys Ser Arg Lys Ala Tyr Val Arg Ile
                165   170   175

Ala Tyr Leu Arg Lys Thr Phe Glu Gln Glu Pro Leu Gly Lys Glu Val
            180   185   190

Ser Leu Glu Gln Glu Val Leu Leu Gln Cys Arg Pro Pro Glu Gly Ile
            195   200   205

Pro Val Ala Glu Val Glu Trp Leu Lys Asn Glu Asp Ile Ile Asp Pro
    210   215   220

Val Glu Asp Arg Asn Phe Tyr Ile Thr Ile Asp His Asn Leu Ile Ile
225   230   235   240

Lys Gln Ala Arg Leu Ser Asp Thr Ala Asn Tyr Thr Cys Val Ala Lys
                245   250   255

Asn Ile Val Ala Lys Arg Lys Ser Thr Thr Ala Thr Val Ile Val Tyr
            260   265   270

Val Asn Gly Gly Trp Ser Thr Trp Thr Glu Trp Ser Val Cys Asn Ser
            275   280   285

Arg Cys Gly Arg Gly Tyr Gln Lys Arg Thr Arg Thr Cys Thr Asn Pro
    290   295   300
```

- 3 -

```
      Ala Pro Leu Asn Gly Gly Ala Phe Cys Glu Gly Gln Ser Val Gln Lys
      305             310             315             320

  5   Ile Ala Cys Thr Thr Leu Cys Pro Val Asp Gly Arg Trp Thr Pro Trp
                      325             330             335

      Ser Lys Trp Ser Thr Cys Gly Thr Glu Cys Thr His Trp Arg Arg Arg
                  340             345             350

 10   Glu Cys Thr Ala Pro Ala Pro Lys Asn Gly Gly Lys Asp Cys Asp Gly
                  355             360             365

      Leu Val Leu Gln Ser Lys Asn Cys Thr Asp Gly Leu Cys Met Gln Ser
                  370             375             380

 15
      Phe Ile Tyr Pro Ile Ser Thr Glu Gln Arg Thr Gln Asn Glu Tyr Gly
      385             390             395             400

      Phe Ser Ser Ala Pro Asp Ser Asp Asp Val Ala Leu Tyr Val Gly Ile
 20               405             410             415

      Val Ile Ala Val Ile Val Cys Leu Ala Ile Ser Val Val Val Ala Leu
                  420             425             430

 25   Phe Val Tyr Arg Lys Asn His Arg Asp Phe Glu Ser Asp Ile Ile Asp
                  435             440             445

      Ser Ser Ala Leu Asn Gly Gly Phe Gln Pro Val Asn Ile Lys Ala Ala
          450             455             460

 30
      Arg Gln Asp Leu Leu Ala Val Pro Pro Asp Leu Thr Ser Ala Ala Ala
      465             470             475             480

      Met Tyr Arg Gly Pro Val Tyr Ala Leu His Asp Val Ser Asp Lys Ile
 35               485             490             495

      Pro Met Thr Asn Ser Pro Ile Leu Asp Pro Leu Pro Asn Leu Lys Ile
                  500             505             510

 40   Lys Val Tyr Asn Thr Ser Gly Ala Val Thr Pro Gln Asp Asp Leu Ser
                  515             520             525

      Glu Phe Thr Ser Lys Leu Ser Pro Gln Met Thr Gln Ser Leu Leu Glu
          530             535             540

 45
      Asn Glu Ala Leu Ser Leu Lys Asn Gln Ser Leu Ala Arg Gln Thr Asp
      545             550             555             560

      Pro Ser Cys Thr Ala Phe Gly Ser Phe Asn Ser Leu Gly Gly His Leu
 50               565             570             575

      Ile Val Pro Asn Ser Gly Val Ser Leu Leu Ile Pro Ala Gly Ala Ile
                  580             585             590

 55   Pro Gln Gly Arg Val Tyr Glu Met Tyr Val Thr Val His Arg Lys Glu
                  595             600             605

      Thr Met Arg Pro Pro Met Asp Asp Ser Gln Thr Leu Leu Thr Pro Val
          610             615             620

 60
      Val Ser Cys Gly Pro Pro Gly Ala Leu Leu Thr Arg Pro Val Val Leu
      625             630             635             640

      Thr Met His His Cys Ala Asp Pro Asn Thr Glu Asp Trp Lys Ile Leu
 65               645             650             655

      Leu Lys Asn Gln Ala Ala Gln Gly Gln Trp Glu Asp Val Val Val Val
                  660             665             670
```

- 4 -

```
      Gly Glu Glu Asn Phe Thr Thr Pro Cys Tyr Ile Gln Leu Asp Ala Glu
              675                 680                 685

 5    Ala Cys His Ile Leu Thr Glu Asn Leu Ser Thr Tyr Ala Leu Val Gly
          690                 695                 700

      His Ser Thr Thr Lys Ala Ala Ala Lys Arg Leu Lys Leu Ala Ile Phe
      705                 710                 715                 720
10
      Gly Pro Leu Cys Cys Ser Ser Leu Glu Tyr Ser Ile Arg Val Tyr Cys
                      725                 730                 735

      Leu Asp Asp Thr Gln Asp Ala Leu Lys Glu Ile Leu His Leu Glu Arg
15                    740                 745                 750

      Gln Thr Gly Gly Gln Leu Leu Glu Glu Pro Lys Ala Leu His Phe Lys
                  755                 760                 765

20    Gly Ser Thr His Asn Leu Arg Leu Ser Ile His Asp Ile Ala His Ser
              770                 775                 780

      Leu Trp Lys Ser Lys Leu Leu Ala Lys Tyr Gln Glu Ile Pro Phe Tyr
      785                 790                 795                 800
25
      His Val Trp Ser Gly Ser Gln Arg Asn Leu His Cys Thr Phe Thr Leu
                      805                 810                 815

      Glu Arg Phe Ser Leu Asn Thr Val Glu Leu Val Cys Lys Leu Cys Val
30                    820                 825                 830

      Arg Gln Val Glu Gly Glu Gly Gln Ile Phe Gln Leu Asn Cys Thr Val
                  835                 840                 845

35    Ser Glu Glu Pro Thr Gly Ile Asp Leu Pro Leu Leu Asp Pro Ala Asn
              850                 855                 860

      Thr Ile Thr Thr Val Thr Gly Pro Ser Ala Phe Ser Ile Pro Leu Pro
      865                 870                 875                 880
40
      Ile Arg Gln Lys Leu Cys Ser Ser Leu Asp Ala Pro Gln Thr Arg Gly
                      885                 890             .     895

      His Asp Trp Arg Met Leu Ala His Lys Leu Asn Leu Asp Arg Tyr Leu
45                    900                 905                 910

      Asn Tyr Phe Ala Thr Lys Ser Ser Pro Thr Gly Val Ile Leu Asp Leu
                  915                 920                 925

50    Trp Glu Ala Gln Asn Phe Pro Asp Gly Asn Leu Ser Met Leu Ala Ala
              930                 935                 940

      Val Leu Glu Glu Met Gly Arg His Glu Thr Val Val Ser Leu Ala Ala
      945                 950                 955                 960
55
      Glu Gly Gln Tyr
```

```
60    <210> 3
      <211> 2780
      <212> DNA
      <213> Homo sapiens

65    <400> 3
      ctgaaaacag aagatagaga ggagtctcgg agctcgccat ctccagcgat ctctacattg 60
      ggaaaaaaca tggagtcagc tccggcagcc cccgaccccg ccgccagcga gccaggcagc 120
      agcggcgcgg acgcggccgc cggctccagg gagaccccgc tgaaccagga atccgcccgc 180
```

- 5 -

```
aagagcgagc cgcctgcccc ggtgcgcaga cagagctatt ccagcaccag cagagatgat 240
gactttttc atgaactccc agaaacttttt ccttctgatc cacctgagcc tctgccacat 300
ttccttattg agcctgaaga agcttatatt gtgaagaata agcctgtgaa cctgtactgt 360
aaagcaagcc ctgccaccca gatctatttc aagtgtaata gtgaatgggt tcatcagaag 420
gaccacatag tagatgaaag agtagatgaa acttccggtc tcattgtccg ggaagtgagc 480
attgagattt cgcgccagca agtggaagaa ctctttggac ctgaagatta ctggtgccag 540
tgtgtggcct ggagctccgc gggtaccaca aagagccgga aggcgtatgt gcgcattgca 600
tatctacgga agacatttga gcaggaaccc ctaggaaagg aagtgtcttt ggaacaggaa 660
gtcttactcc agtgtcgacc acctgaaggg atcccagtgg ctgaggtgga atggttgaaa 720
aatgaagaca taattgatcc cgttgaagat cggaattttt atattactat tgatcacaac 780
ctcatcataa agcaggcccg actctctgat actgcaaatt acacctgtgt tgccaaaaac 840
attgttgcca agaggaaaag tacaactgcc actgtcatag tctatgtcaa cggtggctgg 900
tccacctgga cggagtggtc tgtgtgtaac agccgctgtg acgagggta tcagaaacgt 960
acaaggactt gtaccaaccc ggcaccactc aatggggggtg ccttctgtga agggcagagt 1020
gtgcagaaaa tagcctgtac tacgttatgc ccagtggatg gcaggtggac gccatggagc 1080
aagtggtcta cttgtggaac tgagtgcacc cactggcgca ggagggagtg cacggcgcca 1140
gcccccaaga atggaggcaa ggactgcgac ggcctcgtct tgcaatcaa gaactcgact 1200
gatgggcttt gcatgcagag tttcatttat cccatttcaa ctgaacagag aacccagaat 1260
gaatatggat tttcttctgc tcctgattca gatgatgttg ctctctatgt tgggattgtg 1320
atagcagtga tcgtttgcct ggcgatctct gtagttgtgg ccttgtttgt gtatcggaag 1380
aatcatcgtg actttgagtc agatattatt gactcttcgg cactcaatgg gggctttcag 1440
cctgtgaaca tcaaggcagc aagacaagat ctgctggctg tacccccaga cctcacgtca 1500
gctgcagcca tgtacagagg acctgtctat gccctgcatg acgtctcaga caaaatccca 1560
atgaccaact ctccaattct ggatccactg cccaacctga aaatcaaagt gtacaacacc 1620
tcaggtgctg tcacccccca agatgacctc tctgagtttta cgtccaagct gtcccctcag 1680
atgacccagt cgttgttgga gaatgaagcc ctcagcctga gaaccagag tctagcaagg 1740
cagactgatc catcctgtac cgcatttggc agcttcaact cactgggagg tcaccttatt 1800
gttcccaatt caggagtcag cttgctgatt cccgctgggg ccattcccca agggagagtc 1860
tacgaaatgt atgtgactgt acacaggaaa gaaactatga ggccacccat ggatgactgt 1920
cagacacttt tgacccctgt ggtgagctgc gggcccccag gagctctgct caccccgcccc 1980
gtcgtcctca ctatgcatca ctgcgcagac cccaataccg aggactggaa aatactgctc 2040
ctcgctggag tacagcatcc gagtctactg tctggatgac acccaggatg ccctgaagga 2100
aattttacat cttgagagac agacgggagg acagctccta gaagaaccta aggctcttca 2160
tttttaaaggc agcacccaca acctgcgcct gtcaattcac gatatcgccc attccctctg 2220
gaagagcaaa ttgctggcta aatatcagga aattccatttt taccatgttt ggagtggatc 2280
tcaaagaaac ctgcactgca ccttcactct ggaaagattt agcctgaaca cagtggagct 2340
ggtttgcaaa ctctgtgtgc ggcaggtgga aggagaaggg cagatcttcc agctcaactg 2400
caccgtgtca gaggaaccta ctggcatcga tttgccgctg ctggatcctg cgaacaccat 2460
caccacggtc acggggccca gtgctttcag catccctctc cctatccggc agaagctctg 2520
tagcagcctg gatgccccc agacgagagg ccatgactgg aggatgctgg cccataagct 2580
gaacctggac aggtacttga attactttgc caccaaatcc agcccaactg cgtaatcct 2640
ggatctttgg gaagcacaga acttcccaga tggaaacctg agcatgctgg cagctgtctt 2700
ggaagaaatg ggaagacatg aaacggtggt gtccttagca gcagaagggc agtattaacc 2760
accatgctgg aaggggaaat                                                 2780
```

<210> 4
<211> 669
<212> PRT
<213> Homo sapiens

<400> 4

```
Met Glu Ser Ala Pro Ala Ala Pro Asp Pro Ala Ala Ser Glu Pro Gly
1               5                   10                  15

Ser Ser Gly Ala Asp Ala Ala Ala Gly Ser Arg Glu Thr Pro Leu Asn
            20                  25                  30

Gln Glu Ser Ala Arg Lys Ser Glu Pro Pro Ala Pro Val Arg Arg Gln
        35                  40                  45

Ser Tyr Ser Ser Thr Ser Arg Asp Asp Phe Phe His Glu Leu Pro
    50                  55                  60

Glu Thr Phe Pro Ser Asp Pro Pro Glu Pro Leu Pro His Phe Leu Ile
65                  70                  75                  80

Glu Pro Glu Glu Ala Tyr Ile Val Lys Asn Lys Pro Val Asn Leu Tyr
```

- 6 -

```
                    85                    90                    95

        Cys Lys Ala Ser Pro Ala Thr Gln Ile Tyr Phe Lys Cys Asn Ser Glu
                    100                   105                   110
  5
        Trp Val His Gln Lys Asp His Ile Val Asp Glu Arg Val Asp Glu Thr
                    115                   120                   125

        Ser Gly Leu Ile Val Arg Glu Val Ser Ile Glu Ile Ser Arg Gln Gln
 10                 130                   135                   140

        Val Glu Glu Leu Phe Gly Pro Glu Asp Tyr Trp Cys Gln Cys Val Ala
        145                   150                   155                   160

 15     Trp Ser Ser Ala Gly Thr Thr Lys Ser Arg Lys Ala Tyr Val Arg Ile
                        165                   170                   175

        Ala Tyr Leu Arg Lys Thr Phe Glu Gln Glu Pro Leu Gly Lys Glu Val
                    180                   185                   190
 20
        Ser Leu Glu Gln Glu Val Leu Leu Gln Cys Arg Pro Pro Glu Gly Ile
                    195                   200                   205

        Pro Val Ala Glu Val Glu Trp Leu Lys Asn Glu Asp Ile Ile Asp Pro
 25     210                   215                   220

        Val Glu Asp Arg Asn Phe Tyr Ile Thr Ile Asp His Asn Leu Ile Ile
        225                   230                   235                   240

 30     Lys Gln Ala Arg Leu Ser Asp Thr Ala Asn Tyr Thr Cys Val Ala Lys
                        245                   250                   255

        Asn Ile Val Ala Lys Arg Lys Ser Thr Thr Ala Thr Val Ile Val Tyr
                    260                   265                   270
 35
        Val Asn Gly Gly Trp Ser Thr Trp Thr Glu Trp Ser Val Cys Asn Ser
                    275                   280                   285

        Arg Cys Gly Arg Gly Tyr Gln Lys Arg Thr Arg Thr Cys Thr Asn Pro
 40         290                   295                   300

        Ala Pro Leu Asn Gly Gly Ala Phe Cys Glu Gly Gln Ser Val Gln Lys
        305                   310                   315                   320

 45     Ile Ala Cys Thr Thr Leu Cys Pro Val Asp Gly Arg Trp Thr Pro Trp
                        325                   330                   335

        Ser Lys Trp Ser Thr Cys Gly Thr Glu Cys Thr His Trp Arg Arg Arg
                    340                   345                   350
 50
        Glu Cys Thr Ala Pro Ala Pro Lys Asn Gly Gly Lys Asp Cys Asp Gly
                    355                   360                   365

        Leu Val Leu Gln Ser Lys Asn Cys Thr Asp Gly Leu Cys Met Gln Ser
 55         370                   375                   380

        Phe Ile Tyr Pro Ile Ser Thr Glu Gln Arg Thr Gln Asn Glu Tyr Gly
        385                   390                   395                   400

 60     Phe Ser Ser Ala Pro Asp Ser Asp Asp Val Ala Leu Tyr Val Gly Ile
                        405                   410                   415

        Val Ile Ala Val Ile Val Cys Leu Ala Ile Ser Val Val Val Ala Leu
                    420                   425                   430
 65
        Phe Val Tyr Arg Lys Asn His Arg Asp Phe Glu Ser Asp Ile Ile Asp
                    435                   440                   445
```

```
       Ser Ser Ala Leu Asn Gly Gly Phe Gln Pro Val Asn Ile Lys Ala Ala
           450                 455             460

       Arg Gln Asp Leu Leu Ala Val Pro Pro Asp Leu Thr Ser Ala Ala Ala
    5  465             470                 475         ·       480

       Met Tyr Arg Gly Pro Val Tyr Ala Leu His Asp Val Ser Asp Lys Ile
                       485                 490             495

   10  Pro Met Thr Asn Ser Pro Ile Leu Asp Pro Leu Pro Asn Leu Lys Ile
                   500                 505             510

       Lys Val Tyr Asn Thr Ser Gly Ala Val Thr Pro Gln Asp Asp Leu Ser
               515                 520             525

   15
       Glu Phe Thr Ser Lys Leu Ser Pro Gln Met Thr Gln Ser Leu Leu Glu
           530                 535             540

       Asn Glu Ala Leu Ser Leu Lys Asn Gln Ser Leu Ala Arg Gln Thr Asp
   20  545                 550                 555                 560

       Pro Ser Cys Thr Ala Phe Gly Ser Phe Asn Ser Leu Gly Gly His Leu
                   565                 570                 575

   25  Ile Val Pro Asn Ser Gly Val Ser Leu Leu Ile Pro Ala Gly Ala Ile
                   580                 585                 590

       Pro Gln Gly Arg Val Tyr Glu Met Tyr Val Thr Val His Arg Lys Glu
               595                 600             605

   30
       Thr Met Arg Pro Pro Met Asp Asp Ser Gln Thr Leu Leu Thr Pro Val
           610                 615                 620

       Val Ser Cys Gly Pro Pro Gly Ala Leu Leu Thr Arg Pro Val Val Leu
   35  625                 630                 635                 640

       Thr Met His His Cys Ala Asp Pro Asn Thr Glu Asp Trp Lys Ile Leu
                       645                 650                 655

   40  Leu Leu Ala Gly Val Gln His Pro Ser Leu Leu Ser Gly
                   660                 665
```

```
       <210> 5
   45  <211> 1863
       <212> DNA
       <213> Homo sapiens

       <400> 5
   50  gttttttttt tttttttggt accatagagt tgctctgaaa acagaagata gagggagtct  60
       cggagctcgc atctccagcg atctctacat tgggaaaaaa catggagtca gctccggcag  120
       cccccgaccc cgccgccagc gagccaggca gcagcggcgc ggacgcggcc gccggctcca  180
       gggagacccc gctgaaccag gaatccgccc gcaagagcga gccgcctgcc ccggtgcgca  240
       gacagagcta ttccagcacc agcagaggta tctcagtaac gaagaagaca catacatctc  300
   55  aaattgaaat tattccatgc aagatctgtg gagacaaatc atcaggaatc cattatggtg  360
       tcattacatg tgaaggctgc aagggctttt tcaggagaag tcagcaaagc aatgccacct  420
       actcctgtcc tcgtcagaag aactgtttga ttgatcgaac cagtagaaac cgctgccaac  480
       actgtcgatt acagaaatgc cttgccgtag ggatgtctcg agatgctgta aaatttggcc  540
       gaatgtcaaa aaagcagaga cagcttgt atgcagaagt acagaaacac cggatgcagc  600
   60  agcagcagcg cgaccaccag cagcagcctg gagaggctga gccgctgacg cccacctaca  660
       acatctcggc caacgggctg acggaacttc acgacgacct cagtaactac attgacgggc  720
       acacccctga ggggagtaag gcagactccg ccgtcagcag cttctacctg gacatacagc  780
       cttccccaga ccagtcaggt cttgatatca atggaatcaa accagaacca atatgtgact  840
       acacaccagc atcaggcttc tttcccctact gttcgttcac caacggcgag acttccccaa  900
   65  ctgtgtccat ggcagaatta gaacaccttg cacagaatat atctaaatcg catctggaaa  960
       cctgccaata cttgagagaa gagctccagc agataacgtg gcagaccttt ttacaggaag  1020
       aaattgagaa ctatcaaaac aagcagcggg aggtgatgtg gcaattgtgt gccatcaaaa  1080
       ttacagaagc tatacagtat gtggtggagt ttgccaaacg cattgatgga tttatggaac  1140
```

- 8 -

```
     tgtgtcaaaa tgatcaaatt gtgcttctaa aagcaggttc tctagaggtg gtgtttatca 1200
     gaatgtgccg tgcctttgac tctcagaaca acaccgtgta ctttgatggg aagtatgcca 1260
     gccccgacgt cttcaaatcc ttaggttgtg aagactttat tagctttgtg tttgaatttg 1320
     gaaagagttt atgttctatg cacctgactg aagatgaaat tgcattattt tctgcatttg 1380
  5  tactgatgtc agcagatcgc tcatggctgc aagaaaaggt aaaaattgaa aaactgcaac 1440
     agaaaattca gctagctctt caacacgtcc tacagaagaa tcaccgagaa gatggaatac 1500
     taacaaagtt aatatgcaag gtgtctacat taagagcctt atgtggacga catacagaaa 1560
     agctaatggc atttaaagca atatacccag acattgtgcg acttcatttt cctccattat 1620
     acaggagtt gttcacttca gaatttgagc cagcaatgca aattgatggg taaatgttat 1680
 10  cacctaagca cttctagaat gtctgaagta caaacatgaa aaacaaacaa aaaaattaac 1740
     cgagacactt tatatggccc tgcacagacc tggagcgcca cacactgcac atcttttggt 1800
     gatcggggtc aggcaaagga ggggaaacaa tgaaaacaaa taaagttgaa cttgtttttc 1860
     tca                                                              1863
```

15
```
     <210> 6
     <211> 523
     <212> PRT
20   <213> Homo sapiens

     <400> 6
     Met Glu Ser Ala Pro Ala Ala Pro Asp Pro Ala Ala Ser Glu Pro Gly
      1               5                  10                  15

25   Ser Ser Gly Ala Asp Ala Ala Ala Gly Ser Arg Glu Thr Pro Leu Asn
                  20                  25                  30

     Gln Glu Ser Ala Arg Lys Ser Glu Pro Pro Ala Pro Val Arg Arg Gln
                  35                  40                  45
30
     Ser Tyr Ser Ser Thr Ser Arg Gly Ile Ser Val Thr Lys Lys Thr His
          50                  55                  60

     Thr Ser Gln Ile Glu Ile Ile Pro Cys Lys Ile Cys Gly Asp Lys Ser
35   65                  70                  75                  80

     Ser Gly Ile His Tyr Gly Val Ile Thr Cys Glu Gly Cys Lys Gly Phe
                          85                  90                  95

40   Phe Arg Arg Ser Gln Gln Ser Asn Ala Thr Tyr Ser Cys Pro Arg Gln
                  100                 105                 110

     Lys Asn Cys Leu Ile Asp Arg Thr Ser Arg Asn Arg Cys Gln His Cys
                  115                 120                 125
45
     Arg Leu Gln Lys Cys Leu Ala Val Gly Met Ser Arg Asp Ala Val Lys
          130                 135                 140

     Phe Gly Arg Met Ser Lys Lys Gln Arg Asp Ser Leu Tyr Ala Glu Val
50   145                 150                 155                 160

     Gln Lys His Arg Met Gln Gln Gln Gln Arg Asp His Gln Gln Gln Pro
                      165                 170                 175

55   Gly Glu Ala Glu Pro Leu Thr Pro Thr Tyr Asn Ile Ser Ala Asn Gly
                  180                 185                 190

     Leu Thr Glu Leu His Asp Asp Leu Ser Asn Tyr Ile Asp Gly His Thr
                  195                 200                 205
60
     Pro Glu Gly Ser Lys Ala Asp Ser Ala Val Ser Ser Phe Tyr Leu Asp
          210                 215                 220

     Ile Gln Pro Ser Pro Asp Gln Ser Gly Leu Asp Ile Asn Gly Ile Lys
65   225                 230                 235                 240

     Pro Glu Pro Ile Cys Asp Tyr Thr Pro Ala Ser Gly Phe Phe Pro Tyr
                      245                 250                 255
```

```
        Cys Ser Phe Thr Asn Gly Glu Thr Ser Pro Thr Val Ser Met Ala Glu
                    260             265             270

   5    Leu Glu His Leu Ala Gln Asn Ile Ser Lys Ser His Leu Glu Thr Cys
                    275             280             285

        Gln Tyr Leu Arg Glu Glu Leu Gln Gln Ile Thr Trp Gln Thr Phe Leu
                    290             295             300
  10
        Gln Glu Glu Ile Glu Asn Tyr Gln Asn Lys Gln Arg Glu Val Met Trp
        305             310             315             320

  15    Gln Leu Cys Ala Ile Lys Ile Thr Glu Ala Ile Gln Tyr Val Val Glu
                    325             330             335

        Phe Ala Lys Arg Ile Asp Gly Phe Met Glu Leu Cys Gln Asn Asp Gln
                    340             345             350

  20    Ile Val Leu Leu Lys Ala Gly Ser Leu Glu Val Val Phe Ile Arg Met
                    355             360             365

        Cys Arg Ala Phe Asp Ser Gln Asn Asn Thr Val Tyr Phe Asp Gly Lys
                    370             375             380
  25
        Tyr Ala Ser Pro Asp Val Phe Lys Ser Leu Gly Cys Glu Asp Phe Ile
        385             390             395             400

        Ser Phe Val Phe Glu Phe Gly Lys Ser Leu Cys Ser Met His Leu Thr
  30                405             410             415

        Glu Asp Glu Ile Ala Leu Phe Ser Ala Phe Val Leu Met Ser Ala Asp
                    420             425             430

  35    Arg Ser Trp Leu Gln Glu Lys Val Lys Ile Glu Lys Leu Gln Gln Lys
                    435             440             445

        Ile Gln Leu Ala Leu Gln His Val Leu Gln Lys Asn His Arg Glu Asp
            450             455             460
  40
        Gly Ile Leu Thr Lys Leu Ile Cys Lys Val Ser Thr Leu Arg Ala Leu
        465             470             475             480

        Cys Gly Arg His Thr Glu Lys Leu Met Ala Phe Lys Ala Ile Tyr Pro
  45                485             490             495

        Asp Ile Val Arg Leu His Phe Pro Pro Leu Tyr Lys Glu Leu Phe Thr
                    500             505             510

  50    Ser Glu Phe Glu Pro Ala Met Gln Ile Asp Gly
                    515             520
```

     <210> 7
 55 <211> 1821
     <212> DNA
     <213> Homo sapiens

     <400> 7
 60 ctagattcct ctgtgtttca tacccaggag gtcagggagg gcaccttgta gtgcctgagg 60
     ccccgagagg gttcacagcc acctgagaag tgtttgcagt ctatgggtgt gtgttctttc 120
     tccaagctgt gtcagctgtg ggatggcgtg gagagaaaac aagaaaaagt tgtttccctc 180
     agctctctgc tgaaaaaatg ctcacgggga gtcagtcaac atttggtatc tcagtaacga 240
     agaagacaca tacatctcaa attgaaatta ttccatgcaa gatctgtgga gacaaatcat 300
 65 caggaatcca ttatggtgtc attacatgtg aaggctgcaa gggctttttc aggagaagtc 360
     agcaaagcaa tgccacctac tcctgtcctc gtcagaagaa ctgtttgatt gatcgaacca 420
     gtagaaaccg ctgccaacac tgtcgattac agaaatgcct tgccgtaggg atgtctcgag 480
     atgctgtaaa atttggccga atgtcaaaaa agcagagaga cagcttgtat gcagaagtac 540
```

```
      agaaacaccg gatgcagcag cagcagcgcg accaccagca gcagcctgga gaggctgagc 600
      cgctgacgcc cacctacaac atctcggcca acgggctgac ggaacttcac gacgacctca 660
      gtaactacat tgacgggcac acccctgagg ggagtaaggc agactccgcc gtcagcagct 720
      tctacctgga catacagcct tccccagacc agtcaggtct tgatatcaat ggaatcaaac 780
 5    cagaaccaat atgtgactac acaccagcat caggcttctt tccctactgt tcgttcacca 840
      acggcgagac ttccccaact gtgtccatgg cagaattaga acaccttgca cagaatatat 900
      ctaaatcgca tctggaaacc tgccaatact tgagagaaga gctccagcag ataacgtggc 960
      agaccttttt acaggaagaa attgagaact atcaaaacaa gcagcgggag gtgatgtggc 1020
      aattgtgtgc catcaaaatt acagaagcta tacagtatgt ggtggagttt gccaaacgca 1080
10    ttgatggatt tatggaactg tgtcaaaatg atcaaattgt gcttctaaaa gcaggttctc 1140
      tagaggtggt gtttatcaga atgtgccgtg cctttgactc tcagaacaac accgtgtact 1200
      ttgatgggaa gtatgccagc cccgacgtct tcaaatcctt aggttgtgaa gactttatta 1260
      gctttgtgtt tgaatttgga aagagtttat gttctatgca cctgactgaa gatgaaattg 1320
      cattattttc tgcatttgta ctgatgtcag cagatcgctc atggctgcaa gaaaaggtaa 1380
15    aaattgaaaa actgcaacag aaaattcagc tagctcttca acacgtccta cagaagaatc 1440
      accgagaaga tggaatacta acaaagttaa tatgcaaggt gtctacatta agagtgttat 1500
      gtggacgaca tacagaaaag ctaatggcat ttaaagcaat ataccagac attgtgcgac 1560
      ttcattttcc tccattatac aaggagttgt tcacttcaga atttgagcca gcaatgcaaa 1620
      ttgatgggta aatgttatca cctaagcact tctagaatgt ctgaagtaca aacatgaaaa 1680
20    acaaacaaaa aaattaaccg agacacttta tatggccctg cacagacctg gagcgccaca 1740
      cactgcacat cttttggtga tcggggtcag gcaaggagg ggaaacaatg aaaacaaata 1800
      aagttgaact tgttttttctc a                                           1821
```

25 <210> 8
   <211> 477
   <212> PRT
   <213> Homo sapiens

30 <400> 8
   Met Leu Thr Gly Ser Gln Ser Thr Phe Gly Ile Ser Val Thr Lys Lys
   1   5   10   15

   Thr His Thr Ser Gln Ile Glu Ile Ile Pro Cys Lys Ile Cys Gly Asp
35   20   25   30

   Lys Ser Ser Gly Ile His Tyr Gly Val Ile Thr Cys Glu Gly Cys Lys
           35   40   45

40 Gly Phe Phe Arg Arg Ser Gln Gln Ser Asn Ala Thr Tyr Ser Cys Pro
       50   55   60

   Arg Gln Lys Asn Cys Leu Ile Asp Arg Thr Ser Arg Asn Arg Cys Gln
   65   70   75   80

45 His Cys Arg Leu Gln Lys Cys Leu Ala Val Gly Met Ser Arg Asp Ala
                   85   90   95

   Val Lys Phe Gly Arg Met Ser Lys Lys Gln Arg Asp Ser Leu Tyr Ala
50   100   105   110

   Glu Val Gln Lys His Arg Met Gln Gln Gln Arg Asp His Gln Gln
               115   120   125

55 Gln Pro Gly Glu Ala Glu Pro Leu Thr Pro Thr Tyr Asn Ile Ser Ala
           130   135   140

   Asn Gly Leu Thr Glu Leu His Asp Asp Leu Ser Asn Tyr Ile Asp Gly
60 145   150   155   160

   His Thr Pro Glu Gly Ser Lys Ala Asp Ser Ala Val Ser Ser Phe Tyr
                   165   170   175

   Leu Asp Ile Gln Pro Ser Pro Asp Gln Ser Gly Leu Asp Ile Asn Gly
65   180   185   190

   Ile Lys Pro Glu Pro Ile Cys Asp Tyr Thr Pro Ala Ser Gly Phe Phe
               195   200   205

- 11 -

```
     Pro Tyr Cys Ser Phe Thr Asn Gly Glu Thr Ser Pro Thr Val Ser Met
         210                 215                 220

  5  Ala Glu Leu Glu His Leu Ala Gln Asn Ile Ser Lys Ser His Leu Glu
     225                 230                 235                 240

     Thr Cys Gln Tyr Leu Arg Glu Glu Leu Gln Gln Ile Thr Trp Gln Thr
                     245                 250                 255
 10
     Phe Leu Gln Glu Glu Ile Glu Asn Tyr Gln Asn Lys Gln Arg Glu Val
                 260                 265                 270

 15  Met Trp Gln Leu Cys Ala Ile Lys Ile Thr Glu Ala Ile Gln Tyr Val
             275                 280                 285

     Val Glu Phe Ala Lys Arg Ile Asp Gly Phe Met Glu Leu Cys Gln Asn
         290                 295                 300

 20  Asp Gln Ile Val Leu Leu Lys Ala Gly Ser Leu Glu Val Val Phe Ile
     305                 310                 315                 320

     Arg Met Cys Arg Ala Phe Asp Ser Gln Asn Asn Thr Val Tyr Phe Asp
                     325                 330                 335
 25
     Gly Lys Tyr Ala Ser Pro Asp Val Phe Lys Ser Leu Gly Cys Glu Asp
                 340                 345                 350

     Phe Ile Ser Phe Val Phe Glu Phe Gly Lys Ser Leu Cys Ser Met His
 30              355                 360                 365

     Leu Thr Glu Asp Glu Ile Ala Leu Phe Ser Ala Phe Val Leu Met Ser
         370                 375                 380

 35  Ala Asp Arg Ser Trp Leu Gln Glu Lys Val Lys Ile Glu Lys Leu Gln
     385                 390                 395                 400

     Gln Lys Ile Gln Leu Ala Leu Gln His Val Leu Gln Lys Asn His Arg
                 405                 410                 415
 40
     Glu Asp Gly Ile Leu Thr Lys Leu Ile Cys Lys Val Ser Thr Leu Arg
                 420                 425                 430

 45  Ala Leu Cys Gly Arg His Thr Glu Lys Leu Met Ala Phe Lys Ala Ile
             435                 440                 445

     Tyr Pro Asp Ile Val Arg Leu His Phe Pro Pro Leu Tyr Lys Glu Leu
         450                 455                 460

 50  Phe Thr Ser Glu Phe Glu Pro Ala Met Gln Ile Asp Gly
     465                 470                 475
```

```
     <400> 9
 60  ctgcctttgg agaaagtgga gtgtggcgct tggttgtcgt tatttcttcg gactgcttcg  60
     cggtgcacgg attcagcttc tgcccagtgg ggctttcagc tgtttgcgcg tctctctgtc 120
     cccctcccct cccccggca cacctctgtc tacgatgagg aaaggtctgc gggcgacagc 180
     ggccgctgc ggactgggac tgggatactt gctgcaaatg ctcgtgctac ctgccctggc 240
     cctgctcagc gccagcggca ctggctccgc cgcccaagat gatgactttt ttcatgaact 300
 65  cccagaaact tttccttctg atccacctga gcctctgcca catttcctta ttgagcctga 360
     agaagcttat attgtgaaga ataagcctgt gaacctgtac tgtaaagcaa gccctgccac 420
     ccagatctat ttcaagtgta atagtgaatg ggttcatcag aaggaccaca tagtagatga 480
     aagagtagat gaaacttccg gtctcattgt ccgggaagtg agcattgaga tttcgcgcca 540
```

- 12 -

```
    gcaagtggaa gaactctttg gacctgaaga ttactggtgc cagtgtgtgg cctggagctc 600
    cgcgggtacc acaaagagcc ggaaggcgta tgtgcgcatt gcatatctac ggaagacatt 660
    tgagcaggaa cccctaggaa aggaagtgtc tttggaacag gaagtcttac tccagtgtcg 720
    accacctgaa gggatcccag tggctgaggt ggaatggttg aaaaatgaag acataattga 780
 5  tcccgttgaa gatcggaatt tttatattac tattgatcac aacctcatca taaagcaggc 840
    ccgactctct gatactgcaa attacacctg tgttgccaaa aacattgttg ccaagaggaa 900
    aagtacaact gccactgtca tagtctatgt caacggtggc tggtccacct ggacggagtg 960
    gtctgtgtgt aacagccgct gtggacgagg gtatcagaaa cgtacaagga cttgtaccaa 1020
    cccggcacca ctcaatgggg gtgccttctg tgaagggcag agtgtgcaga aaatagcctg 1080
10  tactacgtta tgcccagtgg atggcaggtg gacgccatgg agcaagtggt ctacttgtgg 1140
    aactgagtgc acccactggc gcaggaggga gtgcacggcg ccagccccca gaatggagg 1200
    caaggactgc gacggcctcg tcttgcaatc caagaactgc actgatgggc tttgcatgca 1260
    gactgctcct gattcagatg atgttgctct ctatgttggg attgtgatag cagtgatcgt 1320
    ttgcctggcg atctctgtag ttgtggcctt gtttgtgtat cggaagaatc atcgtgactt 1380
15  tgagtcagat attattgact cttcggcact caatgggggc tttcarcctg tgaacatcaa 1440
    ggcagcaaga caagatctgc tggctgtacc cccagacctc acgtcagctg cagccatgta 1500
    cagaggacct gtctatgccc tgcatgacgt ctcagacaaa atcccaatga ccaactctcc 1560
    aattctggat ccactgccca acctgaaaat caaagtgtac aacacctcag gtgctgtctc 1620
    cccccaagat gacctctctg agttacgtc caagctgtcc cctcagatga cccagtcgtt 1680
20  gttggagaat gaagccctca gcctgaagaa ccagagtcta gcaaggcaga ctgatccatc 1740
    ctgtaccgca tttggcagct tcaactcgct gggaggtcac cttattgttc ccaattcagg 1800
    agtcagcttg ctgattcccg ctggggccat tccccaaggg agagtctacg aaatgtatgt 1860
    gactgtacac aggaaagaaa ctatgaggcc acccatggat gactctcaga cactttttgac 1920
    ccctgtggtg agctgtgggc ccccaggagc tctgctcacc cgccccgtcg tcctcactat 1980
25  gcatcactgc gcagacccca ataccgagga ctggaaaata ctgctcaaga accaggcagc 2040
    acagggacag tgggaggatg tggtggtggt cggggaggaa aacttcacca cccctgcta 2100
    cattaagctg gatgcagagg cctgccacat cctcacagag aacctcagca cctacgccct 2160
    ggtaggacat tccaccacca agcggctgc aaagcgcctc aagctggcca tctttgggcc 2220
    cctgtgctgc tcctcgctgg agtacagcat ccgagtctac tgtctggatg acacccagga 2280
30  tgccctgaag gaaattttac atcttgagag acagacggga ggacagctcc tagaagaacc 2340
    taaggctctt cattttaaag gcagcaccca caacctcgcg ctgtcaattc acgatatcgc 2400
    ccattccctc tggaagagca aattgctggc taaatatcag gaaattccat tttaccatgt 2460
    ttggagtgga tctcaaagaa acctgcactg caccttcact ctggaaagat ttagcctgaa 2520
    cacagtggag ctggtttgca aactctgtgt gcggcaggtg gaaggagaag gcagatctt 2580
35  ccagctcaac tgcaccgtgt cagaggaacc tactggcatc gatttgccgc tgctggatcc 2640
    tgcgaacacc atcaccacgg tcacggggcc cagtgctttc agcatccctc tccctatccg 2700
    gcagaagctc tgtagcagcc tggatgcccc ccagacgaga ggccatgact ggaggatgct 2760
    ggcccataag ctgaacctgg acaggtactt gaattacttt gccaccaaat ccagcccaac 2820
    tggcgtaatc ctggatcttt gggaagcaca gaacttccca gatggaaacc tgagcatgct 2880
40  ggcagctgtc ttggaagaaa tgggaagaca tgaaacggtg gtgtccttag cagcagaagg 2940
    gcagtattaa ccaccatgct ggaaggggaa atgaaggaca aaatgcaca gggagtctgt 3000
    ggccgtccag gtgaatcaca gctgaggagg aaatccagat gagaccaatg cacttcacag 3060
    gcaagaatgc agcaggagcc agaaggaaaa cagatacaac tgcccatgta catgcccact 3120
    ttactcggag atcatcacgg gagttaagaa aaattgtgta aatttgtacc ttgaatttag 3180
45  ctatcaacct aatttttcctc ttagttgggc tgtatgctgt gtggtacagg atcttacagt 3240
    ttcctaggaa acgctttta ttgctatcca gatatatgga taaacttttct taacaaaccc 3300
    aatttctaca aatgttgttt acatcaaatt ggacaggat gcagacactg tccatggctc 3360
    gttctatttt tgttcaaatc atttgaagtt gaagctgtgg acggtttgtt gtgtctattt 3420
    cagattagta atttacagag aaatcacaga ctttttgctac aaatcgtgtg catcaagtgt 3480
50  ctcagataat cctcccatca gtgttctgtt tctagaactt gtagaaccag tgttactgtt 3540
    tgtatcaggg aagtggagaa tctaagtgta aaaaagaaat aactaagact cctattcctt 3600
    ggagggaccc ttctggtgcc ctttgggaat aaagctgtag cactgc        3646
```

```
55  <210> 10
    <211> 931
    <212> PRT
    <213> Homo sapiens

60  <400> 10
    Met Arg Lys Gly Leu Arg Ala Thr Ala Ala Arg Cys Gly Leu Gly Leu
    1               5                   10                  15

    Gly Tyr Leu Leu Gln Met Leu Val Leu Pro Ala Leu Ala Leu Leu Ser
65                  20                  25                  30

    Ala Ser Gly Thr Gly Ser Ala Ala Gln Asp Asp Asp Phe Phe His Glu
                    35                  40                  45
```

```
      Leu Pro Glu Thr Phe Pro Ser Asp Pro Pro Glu Pro Leu Pro His Phe
          50              55              60

5     Leu Ile Glu Pro Glu Glu Ala Tyr Ile Val Lys Asn Lys Pro Val Asn
          65              70              75              80

      Leu Tyr Cys Lys Ala Ser Pro Ala Thr Gln Ile Tyr Phe Lys Cys Asn
                      85              90              95
10
      Ser Glu Trp Val His Gln Lys Asp His Ile Val Asp Glu Arg Val Asp
                  100             105             110

15    Glu Thr Ser Gly Leu Ile Val Arg Glu Val Ser Ile Glu Ile Ser Arg
              115             120             125

      Gln Gln Val Glu Glu Leu Phe Gly Pro Glu Asp Tyr Trp Cys Gln Cys .
          130             135             140

20    Val Ala Trp Ser Ser Ala Gly Thr Thr Lys Ser Arg Lys Ala Tyr Val
          145             150             155             160

      Arg Ile Ala Tyr Leu Arg Lys Thr Phe Glu Gln Glu Pro Leu Gly Lys
                      165             170             175
25
      Glu Val Ser Leu Glu Gln Glu Val Leu Leu Gln Cys Arg Pro Pro Glu
                  180             185             190

      Gly Ile Pro Val Ala Glu Val Glu Trp Leu Lys Asn Glu Asp Ile Ile
30        195             200             205

      Asp Pro Val Glu Asp Arg Asn Phe Tyr Ile Thr Ile Asp His Asn Leu
          210             215             220

35    Ile Ile Lys Gln Ala Arg Leu Ser Asp Thr Ala Asn Tyr Thr Cys Val
          225             230             235             240

      Ala Lys Asn Ile Val Ala Lys Arg Lys Ser Thr Thr Ala Thr Val Ile
                      245             250             255
40
      Val Tyr Val Asn Gly Gly Trp Ser Thr Trp Thr Glu Trp Ser Val Cys
                  260             265             270

      Asn Ser Arg Cys Gly Arg Gly Tyr Gln Lys Arg Thr Arg Thr Cys Thr
45        275             280             285

      Asn Pro Ala Pro Leu Asn Gly Gly Ala Phe Cys Glu Gly Gln Ser Val
          290             295             300

50    Gln Lys Ile Ala Cys Thr Thr Leu Cys Pro Val Asp Gly Arg Trp Thr
          305             310             315           . 320

      Pro Trp Ser Lys Trp Ser Thr Cys Gly Thr Glu Cys Thr His Trp Arg
                      325             330             335
55
      Arg Arg Glu Cys Thr Ala Pro Ala Pro Lys Asn Gly Gly Lys Asp Cys
                  340             345             350

      Asp Gly Leu Val Leu Gln Ser Lys Asn Cys Thr Asp Gly Leu Cys Met
60        355             360             365

      Gln Thr Ala Pro Asp Ser Asp Asp Val Ala Leu Tyr Val Gly Ile Val
          370             375             380

65    Ile Ala Val Ile Val Cys Leu Ala Ile Ser Val Val Val Ala Leu Phe
          385             390             395             400

      Val Tyr Arg Lys Asn His Arg Asp Phe Glu Ser Asp Ile Ile Asp Ser
```

- 14 -

```
                    405                 410                 415
      Ser Ala Leu Asn Gly Gly Phe Gln Pro Val Asn Ile Lys Ala Ala Arg
                420                 425                 430
  5
      Gln Asp Leu Leu Ala Val Pro Pro Asp Leu Thr Ser Ala Ala Ala Met
                435                 440                 445
      Tyr Arg Gly Pro Val Tyr Ala Leu His Asp Val Ser Asp Lys Ile Pro
 10       450                 455                 460
      Met Thr Asn Ser Pro Ile Leu Asp Pro Leu Pro Asn Leu Lys Ile Lys
      465                 470                 475                 480
 15   Val Tyr Asn Thr Ser Gly Ala Val Ser Pro Gln Asp Asp Leu Ser Glu
                    485                 490                 495
      Phe Thr Ser Lys Leu Ser Pro Gln Met Thr Gln Ser Leu Leu Glu Asn
                500                 505                 510
 20
      Glu Ala Leu Ser Leu Lys Asn Gln Ser Leu Ala Arg Gln Thr Asp Pro
                515                 520                 525
      Ser Cys Thr Ala Phe Gly Ser Phe Asn Ser Leu Gly Gly His Leu Ile
 25       530                 535                 540
      Val Pro Asn Ser Gly Val Ser Leu Leu Ile Pro Ala Gly Ala Ile Pro
      545                 550                 555                 560
 30   Gln Gly Arg Val Tyr Glu Met Tyr Val Thr Val His Arg Lys Glu Thr
                    565                 570                 575
      Met Arg Pro Pro Met Asp Asp Ser Gln Thr Leu Leu Thr Pro Val Val
                580                 585           .     590
 35
      Ser Cys Gly Pro Pro Gly Ala Leu Leu Thr Arg Pro Val Val Leu Thr
                595                 600                 605
      Met His His Cys Ala Asp Pro Asn Thr Glu Asp Trp Lys Ile Leu Leu
 40       610                 615                 620
      Lys Asn Gln Ala Ala Gln Gly Gln Trp Glu Asp Val Val Val Val Gly
      625                 630                 635                 640
 45   Glu Glu Asn Phe Thr Thr Pro Cys Tyr Ile Lys Leu Asp Ala Glu Ala
                    645                 650                 655
      Cys His Ile Leu Thr Glu Asn Leu Ser Thr Tyr Ala Leu Val Gly His
                660                 665                 670
 50
      Ser Thr Thr Lys Ala Ala Ala Lys Arg Leu Lys Leu Ala Ile Phe Gly
                675                 680                 685
      Pro Leu Cys Cys Ser Ser Leu Glu Tyr Ser Ile Arg Val Tyr Cys Leu
 55       690                 695                 700
      Asp Asp Thr Gln Asp Ala Leu Lys Glu Ile Leu His Leu Glu Arg Gln
      705                 710                 715                 720
 60   Thr Gly Gly Gln Leu Leu Glu Glu Pro Lys Ala Leu His Phe Lys Gly
                    725                 730                 735
      Ser Thr His Asn Leu Arg Leu Ser Ile His Asp Ile Ala His Ser Leu
                740                 745                 750          .
 65
      Trp Lys Ser Lys Leu Leu Ala Lys Tyr Gln Glu Ile Pro Phe Tyr His
                755                 760                 765
```

- 15 -

```
        Val Trp Ser Gly Ser Gln Arg Asn Leu His Cys Thr Phe Thr Leu Glu
            770             775             780
```

```
        Arg Phe Ser Leu Asn Thr Val Glu Leu Val Cys Lys Leu Cys Val Arg
  5     785             790             795             800
```

```
        Gln Val Glu Gly Glu Gly Gln Ile Phe Gln Leu Asn Cys Thr Val Ser
                        805             810             815
```

```
 10     Glu Glu Pro Thr Gly Ile Asp Leu Pro Leu Leu Asp Pro Ala Asn Thr
                        820             825             830
```

```
        Ile Thr Thr Val Thr Gly Pro Ser Ala Phe Ser Ile Pro Leu Pro Ile
                835             840             845
 15
        Arg Gln Lys Leu Cys Ser Ser Leu Asp Ala Pro Gln Thr Arg Gly His
            850             855             860
```

```
        Asp Trp Arg Met Leu Ala His Lys Leu Asn Leu Asp Arg Tyr Leu Asn
 20     865             870             875             880
```

```
        Tyr Phe Ala Thr Lys Ser Ser Pro Thr Gly Val Ile Leu Asp Leu Trp
                        885             890             895
```

```
 25     Glu Ala Gln Asn Phe Pro Asp Gly Asn Leu Ser Met Leu Ala Ala Val
                    900             905             910
```

```
        Leu Glu Glu Met Gly Arg His Glu Thr Val Val Ser Leu Ala Ala Glu
                915             920             925
 30
        Gly Gln Tyr
                930
```

```
 35     <210> 11
        <211> 6277
        <212> DNA
        <213> Homo sapiens
```

```
 40     <400> 11
        ataaagcaca tttagcattg ttgtgtttta ataactgcaa atgttctaaa tgtgaataag 60
        agcatataat taagattttt tgaataaact cctaaaattg aaatgtttgt gttgtcttta 120
        tatcattacc ctaatgccca tttttggttg aggtatttga cagccagaat aatggctccc 180
        caaggatgtc catggttttg gaatttaaga atatgttaca ttacatggca aatctgtaga 240
 45     aattaaagta gcagatggat ttaaagttgc taatctgctg actttaagag aggtagattt 300
        tcttggatta ttccattggg tccaatatta tcacaataat ttctaaatgt ggaggaaatt 360
        agaagaagtg agtgctttga tacgagaagt acttgaacca tacttgctgg gtgtgaagat 420
        ggggggaaggg gccactagcc aaagaatgta ggtgtcctct ggaagctgga aacagctaga 480
        aaacatgctt tctgtagagg ctgcagaaag gagctcagct ctgggatcat tctcagttcc 540
 50     ttaaggctgc cctctggtcc tagccttggc tagcctaggc cttggccttc tcatagaatc 600
        acaatttatt ttttaaaaag tcatcaagag aattaatctc tcaagcttgc catgatcatg 660
        tcttatgtaa tctaatcaag gaaatggaat atcccctcat atccataagc cctggccaca 720
        ctcaagagaa aaacatatac atggcaaata tagcagagaa caagaaattt ggaggccatc 780
        ttggaattct gtctacaaca ctcctggtat tccctctgtg tgtttgtctt tgtctctctc 840
 55     cacatatata tacgtacata cacatccatg cacatatgta tttgtattac ttttttcaat 900
        gtagacatat cagcttctta taatatttga tttctttgtt tttccactag ttcagtcata 960
        tttcgctgtt ttagctacca gatcccatct gatacatgaa aacaacatga agaagataaa 1020
        gaaagtttct ctatgcatct tttctctcgt gacattcaat tgcatactca ccatcaccca 1080
        aacagcaaaa ttattgactg acacttcaaa taatctcttc taatacttat ttacattaaa 1140
 60     aatatttttc tttatgaggg tgaagtagaa attaattcac agctctgtac tctggacaaa 1200
        gaaaaaactg taacaaaaaa atcttcacac tgatctaaca ctttatattc tcatgagtca 1260
        agtgattaat taaattccaa tgctcctctg aaggaggttg ggcatttcta taattaaaa 1320
        aatatcgccg ggcatggtgg ctcacgtctg taatcccagc actttgggaa gccaaggcag 1380
        gcagatcacg aggtcaggag atcgagacca tcctggctta cacggtgaaa ccctgtctct 1440
 65     actaaaaata caaaaaaaaa aaaagttagg tgggcgtagt ggcgggcgcc tgtagtccca 1500
        gctactcggg aggctgaggc agaagaatgg cgtgaaccca ggaggcggag cttgcagtga 1560
        gccaagatcg tgccactgca ctccagcctg ggtgacagag cgagactcca tctcaaaaaa 1620
        aaaaaaaaaa ttataactaa agttttgaat taaatcattc tgattgtcca ggaatgcaca 1680
```

```
cccttaaata tatgtaataa aaaattaaag atttcttata gaaaaactta ttgaaaaagt 1740
ccctgaaaga taacaaatga tattataaac tatgtatttc tgtagtaaat ttcccaaaaa 1800
tacataattt tatgagcaaa atggtgtgga atatataaaa tattgtatgt atgtgtgtgt 1860
atataagctt tttaagtgaa gttaagaaac atgaatgagg acctatgaag cattatttct 1920
gtgcacgtac caatatcctg ttatttccag tgcccaaccc taagatctct gactctacca 1980
cattaacttc agactaaaaa ctaacccttt taaacacacc gtaaatgatt ttttttttgtt 2040
aaatgcaact taaaaatttc aaaatatata atagtaaaaa tgatgtttaa tatattgtgt 2100
tgaaatgtta aagaataaac tgtagtttga atgcatctga atatttgta ggcatgcaac 2160
agctcttagt aagaaaccat tccatctttc tgagagaaag ttgtatatta actgaagaga 2220
ggcatcttgt tttgatctgg aggcacaaga aatcttaaag tgtgaatccc attaggttat 2280
aagataaaaa aaaatcctat cagagaatag gaaaataaaa accactagta atctcattac 2340
tgcctcttca aatactactg ctatataggt gaacagcttc ccctctagtc tttcctcttt 2400
cttcccaaaa tagccgacga gtggatcaag catgtctagt gggatataag cacaaagtat 2460
gcttattctt gttttctcct ctttttattt gttctgatta ttaatttttc ccctagtcat 2520
agttcttttt ttggatgaaa tttagggcaa gtgttcaggc ttacctagtt acttcagatg 2580
atgacatctc ctctaaacag taattaatat tttcagtcca tggtaatatt caacatttta 2640
agctcattta aaatactaac tatgccccct gatatggttt gactctgtgt ctacacccaa 2700
atctcatgtc aaattgtaat ccccacttat tgaaggtggg gactggtggg aggtgattgg 2760
atcatagtcg ggggttccag tggtttagcg ccatcctccc tagggctgtc ttgtgataga 2820
gttctcacca gatccgatga gatctgatgg tttcaaagtg tgtagcagtc tcagtctctc 2880
tgtctgtctg tctgtctctc tctctgtctc tcaatcccct gctccaccat ggtaagatgt 2940
gcttacttcc cctttatgtt ttgacacgat tgtaagtttc ctgaggcctc ccagccatgc 3000
ttctgtacag cctgaggaac tgtgagtcaa ttaaatgtct tttcttcata aactacccag 3060
tctcaggtag ttctttatag cagcatgaaa acagactaat acaccccctt tctcagcctg 3120
tgcttgtggt aaggctagcc aatgcaagca gaaagagggg tgctgtctgc tgtttctcca 3180
attggcatct gtgccccttc ttcatcttgt cagttatagt gggaggccca agacttactt 3240
ttggcctcag acacagtcaa ggatcatcct gatgcaaaaa acaaaatcac ctttgaacct 3300
cttcctccac accatcttcc actttggttt tccgctatgc ctttgtactg gggacaaaga 3360
ctatccacga atccttactt taaaaactga ggcagtggct ctgaatcatt ccccctttgga 3420
cacccccaca catctgaaca ccctcgtgtc ccaacaccac atctgctgaa gttgactgga 3480
cctgaaatgc tggaggctca gtgttttcgg aaactgcgga gagttctcct gccacaattc 3540
tcttgttgtc cgtcaaaagc aattacatgt ttcagatgat gaaaagcact gtcatgaaaa 3600
gctggcacag cagccaagga gacagatgta ttaaaccaca cggcttctca gaactcccac 3660
ttacgttgga gctcagcaca gagatgagca tggtgatatc cccccgtcta acatcctccc 3720
atttggattt aatgcatgag gctcgtttct gatgaggtgc caaattcttt cggtggacaa 3780
acacaaagtt gcagaattca gtgatcatac aagtccatgt cctcaaacga aaataataat 3840
actataaatg caaagatgct accataaaaa atacagtagg tggacttttg tgagtcaaca 3900
taaaaaaatc cagcattttct aactggtagc atgaggagta ccagtctgca ggatgttaac 3960
gcactgatag gctatggaca atatattcca cacttacgga agtggggaaa ctataggtca 4020
gacaaagcta caggtacttc tttctttctt ttttctttttt ttctttctga gatggagtct 4080
ccctctgtcg cctaggctgg agtgcaatgg catgatctca gctcactgca acctccgcct 4140
cccgggttca agtgattctc ctgcctcagc ctcctgagtc gctgggatta taggcgcaca 4200
ccaccaacca cccggctaat tttatatt tttagtagaa acgaggtttc actgtgttag 4260
ccagaatggt ctcgaactcc tgacctaggt gatctgcctg cctcagcctc ccaaagtgct 4320
gggattacag gtgtgagcca cggcactcgg cccaagtact tcttaactgc aggacttctc 4380
agaggctttt aatatggtaa tgagtgctgt gcagtgagat gactcaaatc aatatatagc 4440
caacacgttt gatatgacca cagaacccat ttccctgaac actttttatc acctcctaga 4500
gcaggggtca gaaaactact gcccatgtgg tctgatctgg ccactgcttg ttttcgtaaa 4560
ttttcactgc ccacagccaa cctcatttgt gtacatgccg tccatggctg ctttcacact 4620
gcagccgcag cgatgagtca tgagacacgc accgtggct cacaaagtct aaaatattta 4680
ctctttggcc ctttacgaa aacgtgtaca aactttgtcc tctgaaatat agtttgggaa 4740
cctacttcac tcatgatatc aataattcta aaaaatttca aacaattttt aaagtcaaca 4800
ttgagaagtt ttccatggtt agaatttaat aattacagtc aataactctc ttaaagcatc 4860
gtgacaataa agtagaagga cactgtgtaa ttctatatgg tctctgtctt cagggagctc 4920
ccaagctagt ttgtgaaaaa gagaactcaa ggcacaaaca actgggggggc aagagatgtt 4980
ctaaacacta agaggaggca atatggcata gtagaaagaa tgcaagcatg tgtaagagta 5040
aaacatacac agggcgcaga gtcacaagag tcaggggttg gtcttggctg tgataccttc 5100
tcctgcgata agagtaagac ctgctttatt gagcacttac tatgtgccag gcaccatccc 5160
agttgctttc catgaaggat tgctctttaa ttcttatcat aatgaatagg tactattatt 5220
atcccagttt atgggtgagg aaaccaagtc ttaggttgac taacttatta aaataaagca 5280
cataccctagt aggtggtgaa caagagccaa aacaagtctg ttggtcagct aaccaccacg 5340
ttatagtggc tgctgcttag gggcagcata tatcctctgc atttccccag aggtgacaga 5400
agtagtggag agggtagtgc tctctaggct ctgacacaca gcccatgttt gctgactcaa 5460
caaccacaca acgtaatgct atggcacctc aggtggcagg gagggtatcg tgggctggac 5520
tgatcttcag aaggctgcat ctgagcgaca tgtggaagga tggcagaagg aagaggggag 5580
tgaggcactc agggtagaca gaaggtgata ctgccacatc ctccactcag aaggaatctg 5640
gaaggttttg acaaàtatgt acattttgga gtgggaacag cagaaagtag gggctggcta 5700
cctactttcc actaccccta tccccactcc ccctaggggg tgaggcagag ataagcacgc 5760
```

- 17 -

```
tttgtggggc acactgatcc acaaacttgc aagcctgagc tccactcagc agcagcctgg 5820
gcaggatgaa tggtggtgtg caggtgtttg cggcatgcat agcttctctt tctcctagag 5880
tcaatccagt gatcccctgc gaaaagaatc ctccacttga cctgaatgct ctgtattggc 5940
accttctgga caggaatcct atcgggtatt tcatcaaagc atcccacagc agttttaagt 6000
gtggctccat gagagtaaga caccaggaca gctgtgccac ctagtgatgc ttgcctgtac 6060
tgtctgcatc ccagagagtg ggagaggctt cggaaaggac tggtattgc tatttttggc 6120
caacacttct acatgcaaag gaatctgaag tctccgcctg ggcttcaaaa catttcttgt 6180
ggcctcactg accattcccg tgagcctcag gggacatgag tgtcttcaag ctaagaggga 6240
gcagtccaac tctgcagcac gaattaccaa ggaacat                           6277
```

```
<210>  12
<211>  1829
<212>  DNA
<213>  Homo sapiens

<400>  12
ttttgccttg gttttcccag ctattaaaag ggagatatca tcattcattc aacaagcatt 60
tcttgcggac ccattttcca cgacagaacc atccaaacca agacacttct tcctattgtg 120
gcaaaaatga gcaacgttaa aactccccag aatgcagagg tgactcacgt gtttatgtaa 180
gtaagcattt agatatggct ttggaaaaga aaacacacac ctaaaagagg ctaccagcat 240
ttgaataaag tgtgtaacct gggtgttcaa aactgtacaa cagtttctgt gtactttaag 300
tcactatcct tcatacttct tccctttaaa ttctatttga aactaaataa tatcaacaat 360
actttaagta agattatgct ggtgttactg atgaaattat atgcaggtct gcttggcctg 420
ttctcatgcg taagcctttg ataacttgtt cctaggttat ccagtctgc ttacctgagt 480
acccacttta tcccagaaac gagacctgaa cactgtgtcc tggtttcatc tttccagtga 540
gccagccttc tgaggcatta gcggctcagc aagaccatgg aggtgagaga ggcacaggca 600
cactccagat gcagggtctc tgccctctgt caagagtcac acggcagaga ggacaagact 660
cctgtcccgg gggaactgtt tttccttttg ccccacaccc cagatatctt cgtgcagcc 720
cctgccctga aagcccggtg agcgtcatgg cggagaagcc agcctgtttc cgattattct 780
gcctgacagg gactatctgc tgctgtgtgc agttgtagaa atgtcataag ctcaggactc 840
aggacacttt gacgtcgagt ccaacaggac ccatagagtc cccctgaaca attctcatct 900
gtgtgggaag cctaaggggt ggttttaagt aggggctggc aggagagtga ggtctgggct 960
gcttctttac ggctcttcaa gtgccggcca tttcctggga ttcccaggag taagtcttga 1020
ctcccatgaa tcccactgac ccctaagtgg catgggaaag gagaggacaa aaagaaagga 1080
gttagacatt tgactaatac tgttcagagt tgaaatgcgc tctttgagca ggtaggcatt 1140
taaagctaac ttttcctcat gggatacact tgtgggttct ttggagactg atctgcgtga 1200
ccccaatggc tcaacgagaa tcttctccta caattccctt gactaggtaa tgccctcact 1260
ctcctgctat cttcttctcc ctggttctca gtgtttcact gccacataaa ctctctctct 1320
cactgttggg gtcccattgc ccctctgagt ggaattcctg ggcaaaagat tcaatgcaag 1380
ctcaccaggc tatctcacat tgggcctaca tctggtctcc tggaaatatg cccatatcct 1440
ttgtctggac aatcctgaga cagacccagc ccaatgcaga agtgcctatt cttctctcag 1500
cagcagatta acttgtctgg gagttactca tcctcagact tctcaagctc attccgacac 1560
ctgtccacct aatgcagcaa ctgcacgtga cacaataaac acttaatgca agtcacaaat 1620
gggagtcaca tatataatat tattagtagc cacgctagaa aaatgagaca gaaacagata 1680
aagttaattt caatttcagt aacatttcat ttaatctaat ctgtcaaaaa tactattgtc 1740
tcaatatata atcaacaaaa ctgttaatga aatacattac agttttttg tattaagtct 1800
ttgaaatgga gtgtgtattt tagacttaa                                    1829
```

```
<210>  13
<211>  2612
<212>  DNA
<213>  Homo sapiens

<400>  13
atgaggaaag gtctgcgggc gacagcggcc cgctgcggac tgggactggg atacttgctg 60
caaatgctcg tgctacctgc cctggccctg ctcagcgcca gcggcactgg ctccgccgcc 120
caagatgatg acttttttca tgaactccca gaaacttttc cttctgatcc acctgagcct 180
ctgccacatt tccttattga gcctgaagaa gcttatattg tgaagaataa gcctgtgaac 240
ctgtactgta aagcaagccc tgccacccag atctatttca agtgtaatag tgaatgggtt 300
catcagaagg accacatagt agatgaaaga gtagatgaaa cttccggtct cattgtccgg 360
gaagtgagca ttgagatttc gcgccagcaa gtggaagaac tctttggacc tgaagattac 420
tggtgccagt gtgtggcctg gagctccgcg ggtaccacaa agagccggaa gcgcgtatgtg 480
cgcattgcat atctacggaa gacatttgag caggaacccc taggaaagga agtgtctttg 540
gaacaggaag tcttactcca gtgtcgacca cctgaaggga tcccagtggc tgaggtggaa 600
tggttgaaaa atgaagacat aattgatccc gttgaagatc ggaatttta tattactatt 660
gatcacaacc tcatcataaa gcaggcccga ctctctgata ctgcaaatta cacctgtgtt 720
```

- 18 -

```
          gccaaaaaca ttgttgccaa gaggaaaagt acaactgcca ctgtcatagt ctatgtcaac 780
          ggtggctggt ccacctggac ggagtggtct gtgtgtaaca gccgctgtgg acgagggtat 840
          cagaaacgta caaggacttg taccaacccg gcaccactca atggggggtgc cttctgtgaa 900
          gggcagagtg tgcagaaaat agcctgtact acgttatgcc cagtggatgg caggtggacg 960
 5        ccatggagca agtggtctac ttgtggaact gagtgcaccc actggcgcag gagggagtgc 1020
          acggcgccag cccccaagaa tggaggcaag gactgcgacg gcctcgtctt gcaatccaag 1080
          aactgcactg atgggctttg catgcagact gctcctgatt cagatgatgt tgctctctat 1140
          gttgggattg tgatagcagt gatcgtttgc ctggcgatct ctgtagttgt ggccttgttt 1200
          gtgtatcgga agaatcatcg tgactttgag tcagatatta ttgactcttc ggcactcaat 1260
10        gggggctttc agcctgtgaa catcaaggca gcaagacaag atctgctggc tgtaccccca 1320
          gacctcacgt cagctgcagc catgtacaga ggacctgtct atgccctgca tgacgtctca 1380
          gacaaaatcc caatgaccaa ctctccaatt ctggatccac tgcccaacct gaaaatcaaa 1440
          gtgtacaaca cctcaggtgc tgtcacccco caagatgacc tctctgagtt tacgtccaag 1500
          ctgtcccctc agatgaccca gtcgttgttg gagaatgaag ccctcagcct gaagaaccag 1560
15        agtctagcaa ggcagactga tccatcctgt accgcatttg gcagcttcaa ctcactggga 1620
          ggtcacctta ttgttcccaa ttcaggagtc agcttgctga ttcccgctgg ggccattccc 1680
          caagggagag tctacgaaat gtatgtgact gtacacagga aagaaactat gaggccacco 1740
          atggatgact ctcagacact tttgacccct gtggtgagct gtgggccccc aggagctctg 1800
          ctcacccgcc ccgtcgtcct cactatgcat cactgcgcag accccaatac cgaggactgg 1860
20        aaaatactgc tcctcgctgg agtacagcat ccgagtctac tgtctggatg acacccagga 1920
          tgccctgaag gaaattttac atcttgagag acagacggga ggacagctcc tagaagaacc 1980
          taaggctctt cattttaaag gcagcaccca caacctgcgc ctgtcaattc acgatatcgc 2040
          ccattccctc tggaagagca aattgctggc taaatatcag gaaattccat tttaccatgt 2100
          ttggagtgga tctcaaagaa acctgcactg caccttcact ctggaaagat ttagcctgaa 2160
25        cacagtggag ctggtttgca aactctgtgt gcggcaggtg gaaggagaag ggcagatctt 2220
          ccagctcaac tgcaccgtgt cagaggaacc tactggcatc gatttgccgc tgctggatcc 2280
          tgcgaacacc atcaccacgg tcacgggggcc cagtgctttc agcatcccto tccctatccg 2340
          gcagaagctc tgtagcagcc tggatgcccc ccagacgaga ggccatgact ggaggatgct 2400
          ggcccataag ctgaacctgg acaggtactt gaattacttt gccaccaaat ccagcccaac 2460
30        tggcgtaatc ctggatcttt gggaagcaca gaacttccca gatggaaacc tgagcatgct 2520
          ggcagctgtc ttggaagaaa tgggaagaca tgaaacggtg gtgtccttag cagcagaagg 2580
          gcagtattaa ccaccatgct ggaagggggaa at                              2612
```

<400> 14

```
Met Arg Lys Gly Leu Arg Ala Thr Ala Ala Arg Cys Gly Leu Gly Leu
 1               5                   10                  15

Gly Tyr Leu Leu Gln Met Leu Val Leu Pro Ala Leu Ala Leu Leu Ser
            20                  25                  30

Ala Ser Gly Thr Gly Ser Ala Ala Gln Asp Asp Asp Phe Phe His Glu
        35                  40                  45

Leu Pro Glu Thr Phe Pro Ser Asp Pro Glu Pro Leu Pro His Phe
    50                  55                  60

Leu Ile Glu Pro Glu Glu Ala Tyr Ile Val Lys Asn Lys Pro Val Asn
65                  70                  75                  80

Leu Tyr Cys Lys Ala Ser Pro Ala Thr Gln Ile Tyr Phe Lys Cys Asn
                85                  90                  95

Ser Glu Trp Val His Gln Lys Asp His Ile Val Asp Glu Arg Val Asp
            100                 105                 110

Glu Thr Ser Gly Leu Ile Val Arg Glu Val Ser Ile Glu Ile Ser Arg
        115                 120                 125

Gln Gln Val Glu Glu Leu Phe Gly Pro Glu Asp Tyr Trp Cys Gln Cys
    130                 135                 140

Val Ala Trp Ser Ser Ala Gly Thr Thr Lys Ser Arg Lys Ala Tyr Val
```

- 19 -

```
      145                 150                 155                 160

      Arg Ile Ala Tyr Leu Arg Lys Thr Phe Glu Gln Glu Pro Leu Gly Lys
                    165             170                 175
  5
      Glu Val Ser Leu Glu Gln Glu Val Leu Leu Gln Cys Arg Pro Pro Glu
                    180             185                 190

      Gly Ile Pro Val Ala Glu Val Glu Trp Leu Lys Asn Glu Asp Ile Ile
 10             195             200                 205

      Asp Pro Val Glu Asp Arg Asn Phe Tyr Ile Thr Ile Asp His Asn Leu
            210             215             220

 15   Ile Ile Lys Gln Ala Arg Leu Ser Asp Thr Ala Asn Tyr Thr Cys Val
      225                 230             235                 240

      Ala Lys Asn Ile Val Ala Lys Arg Lys Ser Thr Thr Ala Thr Val Ile
                    245             250                 255
 20
      Val Tyr Val Asn Gly Gly Trp Ser Thr Trp Thr Glu Trp Ser Val Cys
                    260             265                 270

      Asn Ser Arg Cys Gly Arg Gly Tyr Gln Lys Arg Thr Arg Thr Cys Thr
 25             275             280             285

      Asn Pro Ala Pro Leu Asn Gly Gly Ala Phe Cys Glu Gly Gln Ser Val
            290             295             300

 30   Gln Lys Ile Ala Cys Thr Thr Leu Cys Pro Val Asp Gly Arg Trp Thr
      305             310             315                 320

      Pro Trp Ser Lys Trp Ser Thr Cys Gly Thr Glu Cys Thr His Trp Arg
                    325             330                 335
 35
      Arg Arg Glu Cys Thr Ala Pro Ala Pro Lys Asn Gly Gly Lys Asp Cys
                    340             345             350

      Asp Gly Leu Val Leu Gln Ser Lys Asn Cys Thr Asp Gly Leu Cys Met
 40             355             360             365

      Gln Thr Ala Pro Asp Ser Asp Val Ala Leu Tyr Val Gly Ile Val
            370             375             380

 45   Ile Ala Val Ile Val Cys Leu Ala Ile Ser Val Val Val Ala Leu Phe
      385             390             395                 400

      Val Tyr Arg Lys Asn His Arg Asp Phe Glu Ser Asp Ile Ile Asp Ser
                    405             410                 415
 50
      Ser Ala Leu Asn Gly Gly Phe Gln Pro Val Asn Ile Lys Ala Ala Arg
                    420             425             430

      Gln Asp Leu Leu Ala Val Pro Pro Asp Leu Thr Ser Ala Ala Ala Met
 55             435             440             445

      Tyr Arg Gly Pro Val Tyr Ala Leu His Asp Val Ser Asp Lys Ile Pro
            450             455             460

 60   Met Thr Asn Ser Pro Ile Leu Asp Pro Leu Pro Asn Leu Lys Ile Lys
      465             470             475                 480

      Val Tyr Asn Thr Ser Gly Ala Val Thr Pro Gln Asp Asp Leu Ser Glu
                    485             490                 495
 65
      Phe Thr Ser Lys Leu Ser Pro Gln Met Thr Gln Ser Leu Leu Glu Asn
                    500             505             510
```

```
      Glu Ala Leu Ser Leu Lys Asn Gln Ser Leu Ala Arg Gln Thr Asp Pro
              515             520             525

      Ser Cys Thr Ala Phe Gly Ser Phe Asn Ser Leu Gly Gly His Leu Ile
  5       530             535             540

      Val Pro Asn Ser Gly Val Ser Leu Leu Ile Pro Ala Gly Ala Ile Pro
      545             550             555             560

 10   Gln Gly Arg Val Tyr Glu Met Tyr Val Thr Val His Arg Lys Glu Thr
                  565             570             575

      Met Arg Pro Pro Met Asp Asp Ser Gln Thr Leu Leu Thr Pro Val Val
              580             585             590
 15
      Ser Cys Gly Pro Pro Gly Ala Leu Leu Thr Arg Pro Val Val Leu Thr
              595             600             605

      Met His His Cys Ala Asp Pro Asn Thr Glu Asp Trp Lys Ile Leu Leu
 20       610             615             620

      Leu Ala Gly Val Gln His Pro Ser Leu Leu Ser Gly
      625             630             635

 25
      <210> 15
      <211> 28
      <212> DNA
      <213> Artificial Sequence
 30
      <220>
      <223> Description of Artificial Sequence: Forward Primer
            MF402L11I

 35   <400> 15
      atggagactt cgctcactgg tcctctttt                              28


      <210> 16
 40   <211> 28
      <212> DNA
      <213> Artificial Sequence

      <220>
 45   <223> Description of Artificial Sequence:Reverse   Primer
            MF402L11I

      <400> 16
      cctggaggca cataaaccct agacatcc                               28
 50

      <210> 17
      <211> 21
      <212> DNA
 55   <213> Artificial Sequence

      <220>
      <223> Description of Artificial Sequence: Forward Primer
            MF402L11II
 60
      <400> 17
      acatcctgag gtaggtggtc c                                      21


 65   <210> 18
      <211> 21
      <212> DNA
      <213> Artificial Sequence
```

```
     <220>
     <223> Description of Artificial Sequence:Reverse Primer
           MF402L11II
5
     <400> 18
     gggtctcact cattctgttg c                                    21


10  <210> 19
    <211> 21
    <212> DNA
    <213> Artificial Sequence

15  <220>
    <223> Description of Artificial Sequence: Forward Primer
          MF402L11III

    <400> 19
20  ctgtattttg actcaattgt g                                     21


    <210> 20
    <211> 21
25  <212> DNA
    <213> Artificial Sequence

    <220>
    <223> Description of Artificial Sequence: Reverse
30         Primer MF402L11III

    <400> 20
    ccaaaagcct ctccttatta c                                     21

35
    <210> 21
    <211> 28
    <212> DNA
    <213> Artificial Sequence
40
    <220>
    <223> Description of Artificial Sequence: Forward Primer
          MF402L11IV

45  <400> 21
    gaatacagac acacagagac agcacctt                               28


    <210> 22
50  <211> 28
    <212> DNA
    <213> Artificial Sequence

    <220>
55  <223> Description of Artificial Sequence: Reverse Primer
          MF402L11IV

    <400> 22
    gttccttgct ccagtgaaag acataatc                               28
60

    <210> 23
    <211> 28
    <212> DNA
65  <213> Artificial Sequence

    <220>
    <223> Description of Artificial Sequence: Forward Primer
```

MF402L11V

<400> 23
ctaacaccag ttcagtggaa cccattgc   28

<210> 24
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Reverse Primer
      MF402L11V

<400> 24
atttgatgtt catacagggt tgggggac   28

<210> 25
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Forward Primer
      MF402L11VI

<400> 25
ctccacttgg actctgatga caccactg   28

<210> 26
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Reverse Primer
      MF402L11VI

<400> 26
catagttcac tgcagcctca acctcct   27

<210> 27
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Forward Primer
      MF90A19I

<400> 27
taattatgat tagacagacc gtcctcca   28

<210> 28
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Reverse Primer
      MF90A19I

<400> 28

```
agtttactac tcagcctttg ccttcact                              28
```

```
<210> 29
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Forward Primer
      MF90A19II

<400> 29
tctgccccac gtccaatcta ggtaactt                              28
```

```
<210> 30
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Reverse Primer
      MF90A19II

<400> 30
gatggtgtgg aggaagaggt tcaaaggt                              28
```

```
<210> 31
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Forward Primer
      MF90A19III

<400> 31
aactgagaac tggaaggtag ctttggga                              28
```

```
<210> 32
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Reverse Primer
      MF90A19III

<400> 32
acaagagcag tcagaactat ttggccct                              28
```

```
<210> 33
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Forward Primer
      MF90A19IV

<400> 33
atttgctggc tccgacagta agtattcc                              28
```

- 24 -

```
<210> 34
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Reverse Primer
      MF90A19IV

<400> 34
atgcagtgat gcttaacacc ctgtctct                          28


<210> 35
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Forward Primer
      MF90A19V

<400> 35
cctgctctgt ctgccttgga aaagaaat                          28


<210> 36
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Reverse Primer
      MF90A19V

<400> 36
tcttggccca gacggtataa gagtccat                          28


<210> 37
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Forward Primer
      MF90A19VI

<400> 37
agtgcaccag taagcatgcc ttccaata                           28


<210> 38
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Reverse Primer
      MF90A19VI

<400> 38
aagctggcaa ggagattctc aaaagtgg                           28


<210> 39
<211> 28
<212> DNA
```

```
     <213> Artificial Sequence

     <220>
     <223> Description of Artificial Sequence: Forward Primer
 5        MF90A19VII

     <400> 39
     accacatctg ctgaagttga ctggacct                              28

10
     <210> 40
     <211> 28
     <212> DNA
     <213> Artificial Sequence
15
     <220>
     <223> Description of Artificial Sequence: Reverse Primer
          MF90A19VII

20   <400> 40
     tctgggcaac atagtgaaac cctgtctc                              28


     <210> 41
25   <211> 28
     <212> DNA
     <213> Artificial Sequence

     <220>
30   <223> Description of Artificial Sequence: Forward Primer
          MF90A19VIII

     <400> 41
     cttgaaccta ggagacggag gttgcagt                              28
35

     <210> 42
     <211> 28
     <212> DNA
40   <213> Artificial Sequence

     <220>
     <223> Description of Artificial Sequence: Reverse Primer
          MF90A19VIII
45
     <400> 42
     aagcatatct ctgaccctct ggccattc                              28


50   <210> 43
     <211> 28
     <212> DNA
     <213> Artificial Sequence

55   <220>
     <223> Description of Artificial Sequence: Forward Primer
          MF90A19IX

     <400> 43
60   gaagctgcaa tcccatcctt gtctcttt                              28


     <210> 44
     <211> 28
65   <212> DNA
     <213> Artificial Sequence

     <220>
```

- 26 -

```
<223> Description of Artificial Sequence: Reverse Primer
      MF90A19IX

<400> 44
tggtggtgca cacctgtaat accagcta                              28


<210> 45
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Forward Primer
      C4P3F

<400> 45
aggatgtcca tggttttgga                                       20


<210> 46
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Reverse Primer
      C4P3R

<400> 46
ctgtttccag cttccagagg                                       20


<210> 47
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Forward Primer
      C4P4F

<400> 47
catggtccca aagctctgtt                                       20


<210> 48
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Reverse Primer
      C4P4R

<400> 48
tgacggaatt tcagtgcaac                                       20


<210> 49
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Forward Primer
      C4P7F
```

```
<400> 49
tctgatacag gggatttggc                                        20


5  <210> 50
   <211> 20
   <212> DNA
   <213> Artificial Sequence

10 <220>
   <223> Description of Artificial Sequence: Reverse Primer
         C4P7R

   <400> 50
15 ttcaggtggg tgatgtgtgt                                       20


   <210> 51
   <211> 20
20 <212> DNA
   <213> Artificial Sequence

   <220>
   <223> Description of Artificial Sequence: Forward Primer
25       C4P8F

   <400> 51
   aggaaagagg ggtgctgtct                                       20

30
   <210> 52
   <211> 20
   <212> DNA
   <213> Artificial Sequence
35
   <220>
   <223> Description of Artificial Sequence: Reverse Primer
         C4P8R

40 <400> 52
   atagcaggag agtgagggca                                       20


   <210> 53
45 <211> 20
   <212> DNA
   <213> Artificial Sequence

   <220>
50 <223> Description of Artificial Sequence: Forward Primer
         C4P9F

   <400> 53
   ggcccacttt ctggttcata                                       20
55

   <210> 54
   <211> 20
   <212> DNA
60 <213> Artificial Sequence

   <220>
   <223> Description of Artificial Sequence: Reverse Primer
         C4P9R
65
   <400> 54
   tcagccagac cagtgtgaaa                                       20
```

```
    <210> 55
    <211> 20
    <212> DNA
 5  <213> Artificial Sequence

    <220>
    <223> Description of Artificial Sequence: Forward Primer
          C15P1F
10
    <400> 55
    ggtctctgcc ctctgtcaag                                          20


15  <210> 56
    <211> 20
    <212> DNA
    <213> Artificial Sequence

20  <220>
    <223> Description of Artificial Sequence: Reverse Primer
          C15P1R

    <400> 56
25  aggcttccca cacagatgag                                          20


    <210> 57
    <211> 20
30  <212> DNA
    <213> Artificial Sequence

    <220>
    <223> Description of Artificial Sequence: Forward Primer
35        C15P2F

    <400> 57
    cactcttggc acccttaacc                                          20

40
    <210> 58
    <211> 20
    <212> DNA
    <213> Artificial Sequence
45
    <220>
    <223> Description of Artificial Sequence: Reverse Primer
          C15P2R

50  <400> 58
    tttgttctgt cctccccaac                                          20


    <210> 59
55  <211> 20
    <212> DNA
    <213> Artificial Sequence

    <220>
60  <223> Description of Artificial Sequence: Forward Primer
          C15P5F

    <400> 59
    tttcatcaaa gcatcccaca                                          20
65

    <210> 60
    <211> 20
```

- 29 -

```
    <212> DNA
    <213> Artificial Sequence

    <220>
 5  <223> Description of Artificial Sequence: Reverse Primer
        C15P5R

    <400> 60
    tggtaattcg tgctgcagag                                    20
10

    <210> 61
    <211> 20
    <212> DNA
15  <213> Artificial Sequence

    <220>
    <223> Description of Artificial Sequence: Forward Primer
        C15P6F
20
    <400> 61
    cccaaacatt ccaacttcgt                                    20


25  <210> 62
    <211> 20
    <212> DNA
    <213> Artificial Sequence

30  <220>
    <223> Description of Artificial Sequence: Reverse Primer
        C15P6R

    <400> 62
35  tagctcaagc ctgaacccat                                    20


    <210> 63
    <211> 26
40  <212> DNA
    <213> Artificial Sequence

    <220>
    <223> Description of Artificial Sequence: Forward Primer
45      BPC4F

    <400> 63
    accctaatgc ccatttttgg ttgagg                             26

50
    <210> 64
    <211> 28
    <212> DNA
    <213> Artificial Sequence
55
    <220>
    <223> Description of Artificial Sequence: Reverse Primer
        BPC15R

60  <400> 64
    aaataccagt cctttccgaa gcctctcc                           28


    <210> 65
65  <211> 28
    <212> DNA
    <213> Artificial Sequence
```

```
     <220>
     <223> Description of Artificial Sequence: Forward Primer
           BPC15F

 5   <400> 65
     cgacagaacc atccaaacca agacactt                                28


     <210> 66
10   <211> 28
     <212> DNA
     <213> Artificial Sequence

     <220>
15   <223> Description of Artificial Sequence: Reverse Primer
           BPC4R

     <400> 66
     gtgtttattg tgtcacgtgc agttgctg                                28
20

     <210> 67
     <211> 27
     <212> DNA
25   <213> Artificial Sequence

     <220>
     <223> Description of Artificial Sequence: Forward Primer
           RORa1 5' UTR
30
     <400> 67
     ctgaaaacag aagatagagg gagtctc                                 27


35   <210> 68
     <211> 20
     <212> DNA
     <213> Artificial Sequence

40   <220>
     <223> Description of Artificial Sequence: Reverse Primer
           UNC5c 3'UTR

     <400> 68
45   atttcccctt ccagcatggt                                        20


     <210> 69
     <211> 27
50   <212> DNA
     <213> Artificial Sequence

     <220>
     <223> Description of Artificial Sequence: Forward Primer
55         AP1

     <400> 69
     ccatcctaat acgactcact atagggc                                 27

60
     <210> 70
     <211> 22
     <212> DNA
     <213> Artificial Sequence
65
     <220>
     <223> Description of Artificial Sequence: Reverse Primer
```

```
     <400> 70
     ctccacagat cttgcatgga at                              22


5    <210> 71
     <211> 23
     <212> DNA
     <213> Artificial Sequence

10   <220>
     <223> Description of Artificial Sequence: Forward Primer
         AP2

     <400> 71
15   actcactata gggctcgagc ggc                             23


     <210> 72
     <211> 23
20   <212> DNA
     <213> Artificial Sequence

     <220>
     <223> Description of Artificial Sequence: Forward Primer
25
     <400> 72
     tctgtgtttc atacccagga ggt                             23


30   <210> 73
     <211> 23
     <212> DNA
     <213> Artificial Sequence

35   <220>
     <223> Description of Artificial Sequence: Reverse Primer

     <400> 73
     agaacacaca cccatagact gca                             23
40

     <210> 74
     <211> 19
     <212> DNA
45   <213> Artificial Sequence

     <220>
     <223> Description of Artificial Sequence: Forward Primer

50   <400> 74
     cctgtaccgc atttggcag                                  19


     <210> 75
55   <211> 20
     <212> DNA
     <213> Artificial Sequence

     <220>
60   <223> Description of Artificial Sequence: Reverse Primer

     <400> 75
     tgcaaaccag ctccactgtg                                 20

65
```